

SEQUENCE LISTING

<110> University of Utah Research Foundation
Adderson, Elisabeth
Bohnsack, John

<120> Isolated Genes for Virulent Group B Streptococcus agalactiae

<130> 1321.2.29

<150> 60/140,084

<151> 1999-06-21

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<170> PatentIn version 3.0

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<212> DNA

<213> Streptococcus agalactiae

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Asn	Lys	Asp	Gly	Ala	Ser	Tyr	Leu	Ile	Pro	Gln	Gly	Lys	Glu	Ala	Glu	
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Tyr	Lys	Ala	Ser	Thr	Asp	Phe	Asn	Ser	Leu	Phe	Thr	Thr	Thr	Thr	Asn	
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gga	ggg	aga	aca	tat	gta	act	aaa	aaa	gat	act	gcg	tca	gca	aat	gag	336
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caa tat gga tat tat tat gtt tct agc act gtt aat aat gga gct gta Gln Tyr Gly Tyr Tyr Tyr Val Ser Ser Thr Val Asn Asn Gly Ala Val 145 150 155 160			480
att atg gtt aca tct gta act cca aat gct act att cat gaa aag aat Ile Met Val Thr Ser Val Thr Pro Asn Ala Thr Ile His Glu Lys Asn 165 170 175			528
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acg tac tcg gtt ggt gat aca gtc aaa tat act att act tat aag aat Thr Tyr Ser Val Gly Asp Thr Val Lys Tyr Thr Ile Thr Tyr Lys Asn 195 200 205			624
gca gtc aat tat cat ggt aca gaa aaa gtg tat caa tat gtt ata aag Ala Val Asn Tyr His Gly Thr Glu Lys Val Tyr Gln Tyr Val Ile Lys 210 215 220			672
gat act atg cca tct gct tct gta gtt gat ttg aac gaa ggg tct tat Asp Thr Met Pro Ser Ala Ser Val Val Asp Leu Asn Glu Gly Ser Tyr 225 230 235 240			720
gaa gta act att act gat gga tca ggg aat att aca act cta act caa Glu Val Thr Ile Thr Asp Gly Ser Gly Asn Ile Thr Thr Leu Thr Gln 245 250 255			768
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aca atc aca gtc act tat aca gga gta tta aag agt gga gct aaa cca Thr Ile Thr Val Thr Tyr Thr Gly Val Leu Lys Ser Gly Ala Lys Pro 305 310 315 320			960
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caa att act ata aaa aaa att gat ggt tcc aca aaa gct tca tta caa	1104
Gln Ile Thr Ile Lys Lys Ile Asp Gly Ser Thr Lys Ala Ser Leu Gln	
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Gly Ala Ile Phe Val Leu Lys Asn Ala Thr Gly Gln Phe Leu Asn Phe	
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Asn Asp Thr Asn Asn Val Glu Trp Gly Thr Glu Ala Asn Ala Thr Glu	
385 390 395 400	
tat aca aca gga gca gat ggt ata att acc att aca ggc ttg aaa gaa	1248
Tyr Thr Thr Gly Ala Asp Gly Ile Ile Thr Ile Thr Gly Leu Lys Glu	
405 410 415	
ggg aca tac tat cta gtt gag aaa aag gct ccc tta ggt tac aat ttg	1296
Gly Thr Tyr Tyr Leu Val Glu Lys Lys Ala Pro Leu Gly Tyr Asn Leu	
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Leu Asp Asn Ser Gln Lys Val Ile Leu Gly Asp Gly Ala Thr Asp Thr	
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act aat tca gat aac ctt tta gtt aac cca act gtt gaa aat aac aaa	1392
Thr Asn Ser Asp Asn Leu Leu Val Asn Pro Thr Val Glu Asn Asn Lys	
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Gly Thr Glu Leu Pro Ser Thr Gly Gly Ile Gly Thr Thr Ile Phe Tyr	
465 470 475 480	
att ata ggt gca att tta gta ata gga gca ggt atc gtg ctt gtt gct	1488
Ile Ile Gly Ala Ile Leu Val Ile Gly Ala Gly Ile Val Leu Val Ala	
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Tyr Lys Val Phe Asp Ala Glu Ile Asp Asn Ala Asn Val Ser Asp Ser
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Asn Lys Asp Gly Ala Ser Tyr Leu Ile Pro Gln Gly Lys Glu Ala Glu
 65 70 75 80

Tyr Lys Ala Ser Thr Asp Phe Asn Ser Leu Phe Thr Thr Thr Thr Asn
 85 90 95

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Ile Ala Thr Trp Ala Lys Ser Ile Ser Ala Asn Thr Thr Pro Val Ser
 115 120 125

Thr Val Thr Glu Ser Asn Asn Asp Gly Thr Glu Val Ile Asn Val Ser
 130 135 140

Gln Tyr Gly Tyr Tyr Tyr Val Ser Ser Thr Val Asn Asn Gly Ala Val
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Ile Met Val Thr Ser Val Thr Pro Asn Ala Thr Ile His Glu Lys Asn
 165 170 175

Thr Asp Ala Thr Trp Gly Asp Gly Gly Gly Lys Thr Val Asp Gln Lys
 180 185 190

Thr Tyr Ser Val Gly Asp Thr Val Lys Tyr Thr Ile Thr Tyr Lys Asn
 195 200 205

Ala Val Asn Tyr His Gly Thr Glu Lys Val Tyr Gln Tyr Val Ile Lys
 210 215 220

Asp Thr Met Pro Ser Ala Ser Val Val Asp Leu Asn Glu Gly Ser Tyr
 225 230 235 240

Glu Val Thr Ile Thr Asp Gly Ser Gly Asn Ile Thr Thr Leu Thr Gln
 245 250 255

Gly Ser Glu Lys Ala Thr Gly Lys Tyr Asn Leu Leu Glu Glu Asn Asn

260

265

270

Asn Phe Thr Ile Thr Ile Pro Trp Ala Ala Thr Asn Thr Pro Thr Gly
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Thr Ile Thr Val Thr Tyr Thr Gly Val Leu Lys Ser Gly Ala Lys Pro
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 325 330 335

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Gln Ile Thr Ile Lys Lys Ile Asp Gly Ser Thr Lys Ala Ser Leu Gln
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Gly Ala Ile Phe Val Leu Lys Asn Ala Thr Gly Gln Phe Leu Asn Phe
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Asn Asp Thr Asn Asn Val Glu Trp Gly Thr Glu Ala Asn Ala Thr Glu
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Tyr Thr Thr Gly Ala Asp Gly Ile Ile Thr Ile Thr Gly Leu Lys Glu
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Thr Asn Ser Asp Asn Leu Leu Val Asn Pro Thr Val Glu Asn Asn Lys
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Gly Thr Glu Leu Pro Ser Thr Gly Gly Ile Gly Thr Thr Ile Phe Tyr
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att ata tcc aag atc ctt cag gta cat att att ata agt atg att cac      96
Ile Ile Ser Lys Ile Leu Gln Val His Ile Ile Ile Ser Met Ile His
          20          25          30

gag ata aag atc ccg act caa cta aag atg cct att ata cga cag ata      144
Glu Ile Lys Ile Pro Thr Gln Leu Lys Met Pro Ile Ile Arg Gln Ile
          35          40          45

cta gtc tca tca aat gtt gat aca aca act aag tac aag tac gta aaa      192
Leu Val Ser Ser Asn Val Asp Thr Thr Thr Lys Tyr Lys Tyr Val Lys
          50          55          60

gac gct tac aaa tta gtc ggt tgg tat tat gtt aat cca tat ggt agt      240
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65          70          75          80

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Ile Arg Pro Tyr Asn Phe Ser Gly Ala Val Thr Gln Asp Ile Asn Leu
          85          90          95

aga gct att tgg cga aag gct gga gat tat cat att ata tac agc aat      336
Arg Ala Ile Trp Arg Lys Ala Gly Asp Tyr His Ile Ile Tyr Ser Asn
          100          105          110

gat gct gtt ggt aca gat gga aag cca gca ttg gat gct tct ggt cag      384
Asp Ala Val Gly Thr Asp Gly Lys Pro Ala Leu Asp Ala Ser Gly Gln
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caa tta caa aca agt aat gag cct act gac cct gat tcc tat gac gat      432
Gln Leu Gln Thr Ser Asn Glu Pro Thr Asp Pro Asp Ser Tyr Asp Asp
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ggc tcc cat tca gcc tta ctg aga cgt ccg aca atg cca gat ggc tat      480
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			180					185					190				
ata	aaa	cct	gtc	att	att	cca	gta	gga	gat	atc	aaa	tta	gaa	gat	acc	624	
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tcc	atc	aaa	tac	aat	ggg	aac	ggg	ggg	act	aga	gta	gaa	aat	ggg	aat	672	
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Thr	Ile	Pro	Glu	Asn	Gln	Tyr	Phe	Thr	Arg	Thr	Gly	Tyr	Asn	Leu	Ile		
			245						250					255			
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Gly	Trp	His	His	Asp	Lys	Asp	Leu	Ala	Asp	Thr	Gly	Arg	Val	Glu	Phe		
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Thr	Leu	Tyr	Ala	Val	Trp	Gln	Pro	Lys	Glu	Tyr	Thr	Val	Gly	Val	Ser		
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aaa	act	gtc	gtt	gga	cta	gat	gaa	gat	aag	acg	aaa	gac	ttc	ttg	ttt	960	
Lys	Thr	Val	Val	Gly	Leu	Asp	Glu	Asp	Lys	Thr	Lys	Asp	Phe	Leu	Phe		
	305				310				315					320			
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Gln	Thr	Lys	Glu	Phe	Lys	Val	Pro	Tyr	Gly	Thr	Ser	Ile	Ser	Ile	Asp		
			340					345					350				
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aat	cta	gca	act	ggg	gaa	gct	gat	aaa	act	tat	gat	gct	acc	ggg	tta	1152	
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Asn Gly Asn Lys Ala Ser His Pro Met Tyr Ser Gly Leu Val Thr Asn				
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Asp Lys Gly Leu Leu Leu Val Asp Ala Asn Asn Tyr Leu Ser Leu Pro				
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Val Gly Lys Tyr Tyr Leu Thr Glu Thr Lys Ala Pro Pro Gly Tyr Leu				
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	485	490	495	
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Thr Phe Glu Gln Asn Gly Asn Asn Ala Thr Pro Ile Lys Glu Asn Leu				
	500	505	510	
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Val Asp Gly Ser Thr Val Tyr Thr Phe Lys Ile Thr Asn Ser Lys Gly				
	515	520	525	
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Thr Glu Leu Pro Ser Thr Gly Gly Ile Gly Thr His Ile Tyr Ile Leu				
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Glu Ile Lys Ile Pro Thr Gln Leu Lys Met Pro Ile Ile Arg Gln Ile
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Asp Ala Tyr Lys Leu Val Gly Trp Tyr Tyr Val Asn Pro Tyr Gly Ser
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Arg Ala Ile Trp Arg Lys Ala Gly Asp Tyr His Ile Ile Tyr Ser Asn
 100 105 110

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Gly Ser His Ser Ala Leu Leu Arg Arg Pro Thr Met Pro Asp Gly Tyr
 145 150 155 160

Arg Phe Arg Gly Trp Trp Tyr Asn Gly Lys Ile Tyr Asn Pro Tyr Asp
 165 170 175

Ser Ile Asp Ile Asp Ala His Leu Ala Asp Ala Asn Lys Asn Ile Thr
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Ser Ile Lys Tyr Asn Gly Asn Gly Gly Thr Arg Val Glu Asn Gly Asn
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Gly Trp His His Asp Lys Asp Leu Ala Asp Thr Gly Arg Val Glu Phe
260 265 270

Thr Ala Gly Gln Ser Ile Gly Ile Asp Asn Asn Leu Asp Ala Thr Asn
275 280 285

Thr Leu Tyr Ala Val Trp Gln Pro Lys Glu Tyr Thr Val Gly Val Ser
290 295 300

Lys Thr Val Val Gly Leu Asp Glu Asp Lys Thr Lys Asp Phe Leu Phe
305 310 315 320

Asn Pro Ser Glu Thr Leu Gln Gln Glu Asn Phe Pro Leu Arg Asp Gly
325 330 335

Gln Thr Lys Glu Phe Lys Val Pro Tyr Gly Thr Ser Ile Ser Ile Asp
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Gln Ser Leu Thr Val Ser Gly Asp Val Asp Ile Ser Phe Thr Asn Thr
385 390 395 400

Arg Ile Lys Gln Lys Val Arg Leu Gln Lys Val Asn Val Glu Asn Asp
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435 440 445

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Val Gly Lys Tyr Tyr Leu Thr Glu Thr Lys Ala Pro Pro Gly Tyr Leu

465

470

475

480

Leu Pro Lys Asn Asp Asp Ile Ser Val Leu Val Ile Ser Thr Gly Val
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Val Asp Gly Ser Thr Val Tyr Thr Phe Lys Ile Thr Asn Ser Lys Gly
 515 520 525

Thr Glu Leu Pro Ser Thr Gly Gly Ile Gly Thr His Ile Tyr Ile Leu
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